nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

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FOI	ali StatiSticai ari	aryses, commit that the following items are present in the figure legend, table legend, main text, or Methods section.						
n/a	Confirmed							
	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement							
	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly							
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.							
	A description of all covariates tested							
	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons							
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)							
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.							
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings							
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes							
	Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated							
		Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.						
So	ftware an	d code						
Poli	cy information a	about <u>availability of computer code</u>						
D	ata collection	PRJEB20773 and PRJNA290380						
D	ata analysis	QIIME 2 ver 2019.4, Deblur, 2013 Greengenes database, SILVA release 138 database, SATé-enabled phylogenetic placement (SEPP), R						

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

package Vegan (vegan: Community Ecology Package), MaAsLin2, R package randomForest

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The study datasets were deposited at the National Center for Biotechnology Information as BioProject PRJNA660912

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🔀 Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences
For a reference copy of t	he document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>
Life scier	nces study design
All studies must dis	close on these points even when the disclosure is negative.
Sample size	We aimed to include at least 50 day care and 20 home care children. We were unable to preform power calculation due to lack of other studies with similar designs (longitudunal day care).
Data exclusions	Exclusion criteria for samples included sample with under 4000reads/saple. We di dnot include samples form subjects treated with antibiotic within 6 weeks of sampling.
Replication	Finding were not replicated due to lack of similar day care study design
Randomization	All day care samples were handled and processed similarly and together and the home care samples were processed with the last day care sampling.
Blinding	Blinding was not relevant

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

	Ma	terials & experimental systems	Methods			
ī	n/a	Involved in the study	n/a	Involved in the study		
	\boxtimes	Antibodies	\boxtimes	ChIP-seq		
	\boxtimes	Eukaryotic cell lines	\boxtimes	Flow cytometry		
	\boxtimes	Palaeontology and archaeology	\boxtimes	MRI-based neuroimaging		
	\boxtimes	Animals and other organisms				
		Human research participants				
	\boxtimes	Clinical data				
	\boxtimes	Dual use research of concern				

Human research participants

Policy information about studies involving human research participants

Population characteristics This is a prospective observational cohort study of 61 children (Male and female) who entered day care in the school year 2018-2019 (September 2018 to July 2019) in 4 different day cares. 24 additional age-matched children in home care setting

were also included. All children were 6month to 4years old.

Four different day care facilities were included, all are located non-rural area in the central part of Israel within 10 kilometers Recruitment

from the lab at the Sheba Medical Center.

Ethical approval for the study was granted by the Sheba Research Ethics Committee Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.